

## AMENDMENTS

### IN THE CLAIMS:

Please amend claims 47, 60 and 63-67, as follows:

D<sup>1</sup>  
Sub E<sup>1</sup>

47. (twice amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a selectable or screenable marker gene [comprising] selected from the group of genes consisting of a dalapon dehalogenase (*deh*) gene[,]; an anthranilate synthase gene that confers resistance to 5 methyl tryptophan[,]; an aequorin gene [, or] and a gene encoding a cell wall protein, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

D<sup>2</sup>

60. (amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a negatively-selectable marker [comprising] selected from the group of genes consisting of a cytosine deaminase gene[,]; a T-DNA gene 2[,]; an antisense *bar* gene; and [or] an antisense *npXII* gene, so that the transgenic plant exhibits one or more characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said marker, and wherein said marker is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

63. (amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding an insect resistance trait [comprising] selected from the group of genes consisting of an oryzacystatin gene[,]; a wheat or barley amylase inhibitor gene[,]; a lipoxygenase gene[,]; an ecdysteroid UDP-glucosyl transferase gene; and [or] a DIMBOA synthetic gene of the *bx* locus, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

D3  
Sub E3

64. (amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a disease resistance trait [comprising] selected from the group of genes consisting of a cecropin gene[,]; a magainin gene; and [or] a pathogenesis related (PR) protein gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

65. (amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a stress resistance trait [comprising] selected from the group of genes consisting of a glycerol-3-phosphate acetyltransferase gene[,]; a superoxide dismutase gene[,]; and [or] a glutathione reductase gene,

so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

3  
D  
66. (amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a drought resistance trait [comprising] selected from the group of genes consisting of a mannitol-1-phosphate dehydrogenase gene[,]; a trehalose-6-phosphate synthase gene[,]; a myoinositol 0-methyltransferase gene; and [or] a Late Embryogenic Protein (LEA) gene, so that the transgenic plant exhibits one or more phenotypic characteristics that render it identifiable over the corresponding untransformed maize plant which does not comprise said gene, and wherein said gene is transmittable through normal sexual reproduction of the transgenic maize plant to subsequent generation plants.

Sub E4  
67. (amended) A fertile, transgenic maize plant, the genome of which has been augmented by the introduction of a DNA composition comprising a gene encoding a grain composition trait [comprising] selected from the group of genes consisting of an aspartokinase gene[,]; an acetyl-CoA carboxylase gene[,]; an ACP-acyltransferase gene[,]; a  $\beta$ -ketoacyl-ACP synthase gene[,]; an acyl carrier protein gene[,]; a fatty acid desaturase gene[,]; a fatty acid epoxidase gene[,]; a fatty acid hydratase gene[,]; a fatty acid dehydratase gene[,]; a sense or antisense phytoene synthase gene[,]; a sense or antisense phytoene desaturase gene[,]; a sense or antisense lycopene